

Load packages.

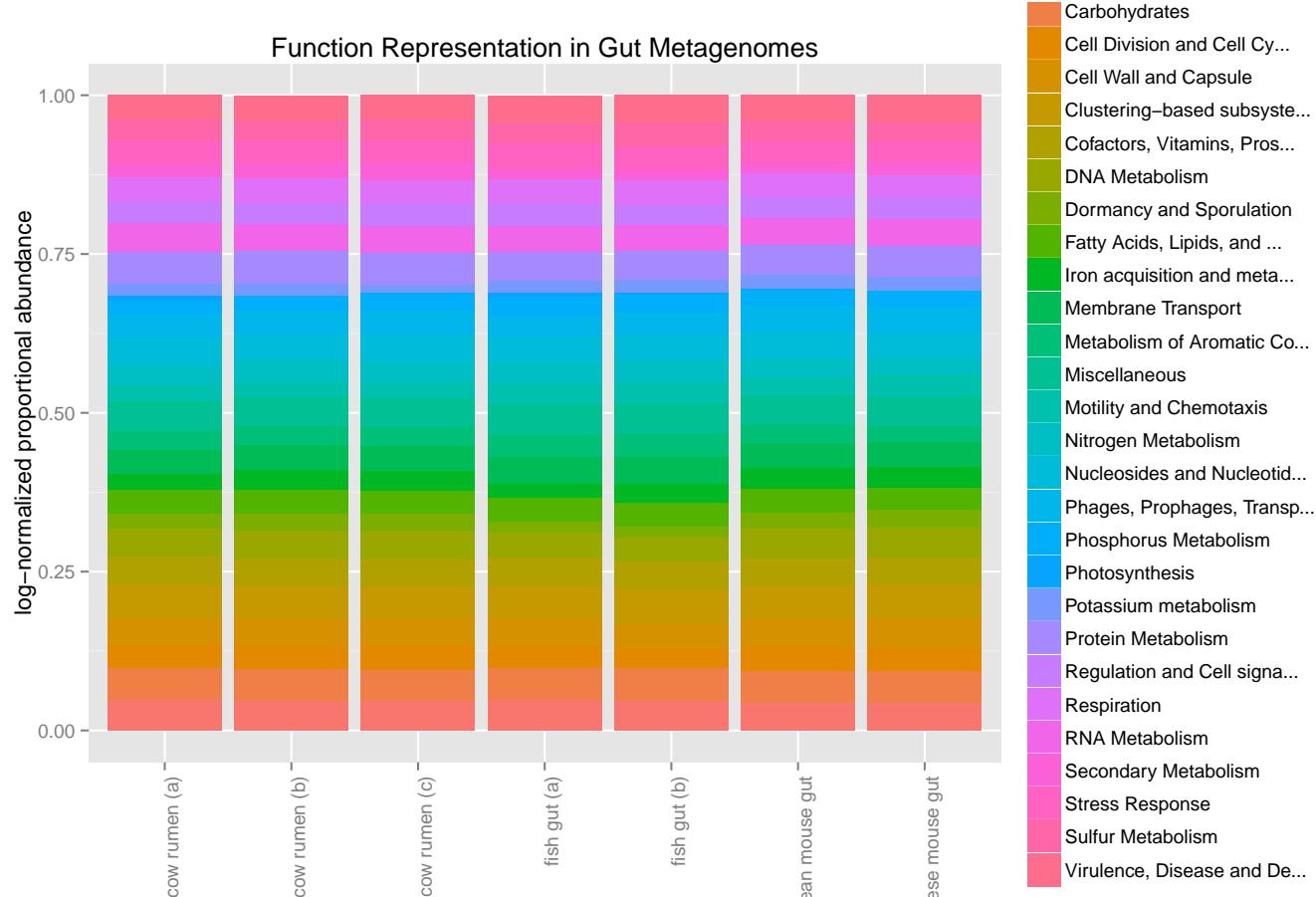
```
> library(matR)
> library(ggplot2)
```

Construct a small metagenome collection, and format data appropriately for ggplot2.

```
> IDs <- c("4441679.3", "4441680.3", "4441682.3",
+   "4441695.3", "4441696.3", "4440463.3", "4440464.3")
> names(IDs) <- c("cow rumen (a)", "cow rumen (b)", "cow rumen (c)",
+   "fish gut (a)", "fish gut (b)", "lean mouse gut", "obese mouse gut")
> cc <- collection(IDs,
+   func1=c(entry="normed", level="level1"),
+   func2=c(entry="normed", level="level2"),
+   func3=c(entry="normed", level="level3"))
> d <- as.data.frame(t(cc$func1))
> r <- reshape(d, vary=list(names(d)), dir="long",
+   ids=rownames(d), times=names(d))
> names(r) <- c("function", "count", "sample")
> rownames(r) <- NULL
```

A simple barchart of normalized taxonomic abundances at the top functional hierarchy level.

```
> ggplot(r[c(3,1,2)]) +
+   geom_bar(aes(x=sample, y=count, fill=`function`),
+   position="fill", stat="identity") +
+   scale_x_discrete(name "") +
+   scale_y_continuous("log-normalized proportional abundance") +
+   labs(title="Function Representation in Gut Metagenomes") +
+   theme(axis.text.x=element_text(angle=90, hjust=1))
```



The samples are very similar, at this function granularity.